

AMENDMENTS TO THE SPECIFICATION

Please replace paragraph [00032] with the following paragraph:

[00032] The method of the present invention has improved efficacy over the previously described methods, *i.e.* it has been shown to provide remarkably reliable predictions (*see* Fig. 8 and Example 1, *infra*) (SEQ ID NO: 128) and it is generally applicable to all biopolymers, including, *inter alia*, RNA, DNA and proteins (*see* Figs. 8-11 and Examples 1-4, *infra*). In particular, the present invention demonstrates improved efficacy over the previously describe methods partly due to: 1) a scoring process that results in scores that are symmetric and uniformly scaled, and/or a process of standardization that results in scores that are uniformly scaled; 2) a rigorous screening process that is intricately linked to its scoring algorithms, such that high accuracy is achieved; 3) a screening process that is neither arbitrary nor absolute, and thus able to implicitly handle the effects of sequence selection, phylogenetic relationships, sequence number; 4) a methodology that does not require preconceived biochemical parameters, or any other type of empirical data such as physicochemical, energetic, similarity descriptors or matrixes and is thus unbiased and not rule-based; 5) a methodology that is highly automated, and does not require enormous amounts of user input; 6) a methodology for evaluating the quality of the input data and suggestion for how to improve it, and is thus a novel method by which to analyze sequence alignments for errors; and 7) a methodology that is iterative, because as the input data is refined via its misalignment algorithm, each successive pass allows for better predictions.

Please replace paragraph [00041] with the following paragraph:

[00041] Figure 8(a) shows the structure for Domain V of the Group II catalytic RNA AI5 γ as predicted by the exemplary embodiment of the method of the present invention (SEQ ID NO: 128) and 8(b) shows the interactions for Domain V of the Group II catalytic RNA AI5 γ according to the biochemically predicted structure (SEQ ID NO: 128);

Please replace paragraph [00046] with the following paragraph:

[00046] Shevek: An exemplary embodiment of the method of the present invention described ~~hereinbelow~~ herein below.

Please replace paragraph [00128] with the following paragraph:

[00128] The steps of the above-described method are preferably performed by a computer. In one preferred embodiment, the computer is a Dell Precision 430 dual processor Pentium III™, 933 [[Mz]] MHz Workstation. Use of the sequence alignment editor software, Se-Al, may be performed on a Power Macintosh 8600/300 Power PC. When the method is performed by a computer, the above-described method steps are embodied in a program storage device readable by a machine, such program storage device including a computer readable medium. Computer readable media include magnetic diskettes, magnetic tapes, optical disks, Read Only Memory, RAM, Direct Access Storage Devices, gate arrays, electrostatic memory, and any other like medium.

[000141] Four sequences were identified as misaligned. These sequences were inspected and edited using the sequence alignment editor program Se-AL, as described previously. Sequences #43 SEQ ID NO:44 (_ZPU16993_cox2) and SEQ ID NO:53 (_BVSCOXII1_cox2_1) were noted to be misaligned and realigned (see Table X). Sequence #16 SEQ ID NO:17 (DRP130746_Dp_nad5) and sequence #73 SEQ ID NO:74 (petB_45_) were noted to be unusual, but not in need of realignment.] The entire Shevek process was then repeated on the altered sequence alignment data set i.e. the process was iterated.

Please replace Table 1 at page 53 with the following table:

		<u>POSITION</u>																									
		1	1	1	1	1	2	2	2	2	2	3	3	3	3	3	4	4	4	4	4						
		0	2	4	6	8	0	2	4	6	8	0	2	4	6	8	0	2	4	6	8	0	2	4	6	8	
<u>Sequence of Interest:</u>																										<u>SEQ</u>	
																										<u>ID NO:</u>	
ai5gamma	----	GAGCCG	TATGCG	AT----	GAAA----	GTCGCACGTACGGTTC--	T	<u>1</u>																			
<u>Functionally Related Sequences:</u>																											
MICLURF1_ndh1__01_	----	GAGCCACATGCAGG----	GAAA----	CTTGACAGTGTGGTTC--	T	<u>2</u>																					
_MIZMCO_cox2_1__02_	----	GAGCTTTTTTGCGGG----	GAAA----	CTTGCAAGTCAAGTTT--	G	<u>3</u>																					
_DCCOXII_cox2_1	----	GAGCTTTTTTGCGGG----	GAAA----	CTTGCAAGTACAGTTT--	G	<u>4</u>																					
_MITACOXII_cox2_1	----	GAGCTTTTTTGCGGG----	GAAA----	CTTGCAAGTCAAGTTT--	G	<u>5</u>																					
MIPHC021_cox2_1	----	GAGCTTTTTTGCGGG----	GAAA----	CTTGCAAGTACAGTTT--	G	<u>6</u>																					
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_MIOS01_Os_cox2	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTAAAGTTT--G	<u>7</u>
_MIHACOXII_cox2	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTACAGTTT--G	<u>8</u>
_MIDBG2IA_nad5_1_03_	---GAGCCGTGTGATGG---GAAA---CCTTCCCGCACGGTTC--G	<u>9</u>
_MTVFNAD5_nad5_1	---GAGCCGTGTGATGG---GAAA---CCTTCCCGCACGGTTC--G	<u>10</u>
MIATNAD5A_nad5_1	---GAGCCGTGTGATGG---GAAA---CCTTCCCGCACGGTTC--G	<u>11</u>
TSP131146_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>12</u>
TRA131145_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>13</u>
ASP130735_Sc_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>14</u>
SAU131147_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>15</u>
AEV130737_Ap_nad5	---GAGCCGTATGCGGG---GAAA---CTTGACAGTGCAGTTT--T	<u>16</u>
DPR130746_Dp_nad5	---GAGCCGTATGCGAA---GAAA---CTTGACAGTGCAGTTT--T	<u>17</u>
ANNAD5_An_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>18</u>
DSP130747_Dd_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>19</u>
SWI131144_nad5	---GAGCCGTATGCGAG---GAAA---CTTGACAGTGCAGTTT--T	<u>20</u>
AF143422_Tc_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>21</u>
AF143423_Pa_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>22</u>
AF143424_Ca_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>23</u>
AF143425_Cp_nad5	---GAGCCGTGTGATGG---GAAA---CCTCCCGCACGGTTC--G	<u>24</u>
MTPACG_nad5_4_08_	---GAGCCGTATGATGG---GAAA---CTATCACGTACGGTTC--G	<u>25</u>
MIATGENA_nad7_1	---TGAGCGCATGCGGG---GAGA---CCCGCACGTACGGTTT--T	<u>26</u>
MIATGENA_nad7_3	---GAGCCGTATGAAGG---GAAA---CTCTCACGTACAGTTT--G	<u>27</u>
_MPOMTCG_nad3	---GAGCCGTGTAATGG---GCAA---CTATTTTCGCACGGTTC--G	<u>28</u>
MIATGENA_nad4_3	---GAGCCTAGTGATAG---GAGA---CTATCTAGCTTGGTTC--G	<u>29</u>
_MPOMTCG_nad4	---GAGCCGTATGCGAG---GAGA---CTTGACAGTACGGTTC--G	<u>30</u>
MISC13_cox1_1_04_	---AAGCCGTATGATGG---GAAA---CTATCACGTACGGTTT--G	<u>31</u>
MTPACG_cox1_1_07_	---GAGCCGTATGCGGT---GAAA---GTCGCACGTACGGTTC--G	<u>32</u>
MTPCCOX1_cox1_1	---GAGCCGTATGCGGT---GAAA---GTCGCACGTACGGTTC--G	<u>33</u>
SPO251292_cox1_1	---GAGCCGTATGCATT---GAAA---GATGCACGTACGGTTC--T	<u>34</u>
MIKLCOX1_cox1_1	---GAGCCGTATGATAT---GAAA---GTATCACGTACGGTTC--G	<u>35</u>
MISC13_cox1_2_05_	---GAGCCGTATGATAT---GAAA---GTATCACGTACGGTTC--G	<u>36</u>
MTPACG_cox1_4_06_	---GAGCCGTATGCAGG---GAAA---CTTGACAGTACGGTTC--G	<u>37</u>
AMU41288_Am_cox1_3	---GAGCCGTATGCGGT---GAAA---GTTGCACGTACGGTTC--G	<u>38</u>
MISPCG_cob_09_	---GAGCCGTATAATTA---CGAAA---GTATCCCGTACGGTTC--G	<u>39</u>
CHNTHX_rps12_10_	---AAGCCGTATTTCGAT---GAAA---GTCGTATGTACGGCTT--G	<u>40</u>
CHSORPS_rps12_2_11_	---AAGCCGTATTTCGAT---GAAA---GTCGTATGTACGGCTT--G	<u>41</u>
CHZMXX_rps12_2_12_	---AAGCCGTATTTCGAT---GAAA---GTCGTATGTACGGCTT--G	<u>42</u>
CHMPXX_rps12_2_13_	---AAGCCGTATTTCGTT---GAAA---ATCGGATGTACGGTTT--G	<u>43</u>
_ZPU16993_cox2	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTCAAGTTT--G	<u>44</u>
AF080087_Ot_rps3	---GAGCCGTGTGATGG---GTGA---CTATCCAGCACGGTTC--G	<u>45</u>
CHNTHX_trnI_14_	---GAGCGCAGTACAAC---GGAGA---GTTGTATGCTGCGTTC--G	<u>46</u>
CHZMXX_trnI_15_	---GAGCGCAGTACAAC---GGGGA---GTTGTATGCTGCGTTC--G	<u>47</u>
CHMPXX_trnI_16_	---GAGCGCAGTACAAC---GGAAA---GTTGTATGCTGCGTTC--G	<u>48</u>
WHTCPTNRI_trnI	---GAGCGCAGTACAAC---GGGGA---GTTGTATGCTGCGTTC--G	<u>49</u>
CHNTHX_trnA_17_	---GAGCACAGTACGAT---GAAA---GTTGTAAGCTGTGTTT--G	<u>50</u>
CHZMXX_trnA_18_	---GAGCACAGTACGAT---GAAA---GTTGTAAGCTGTGTTT--G	<u>51</u>
CHMPXX_trnA_19_	---GAGCACAGTACGAT---GAAA---GTTGTAAGCTGTGTTT--G	<u>52</u>
_BVSCOXIII_cox2_1	---GAGCTTTTTGCGGG---GAAA---CTTGCAAGTACAGTTT--G	<u>53</u>
CHNTHX_trnK_26_	---AAGCCGTGTGCAAT---GAAA---AATGCAAGCACGGCTT--G	<u>54</u>
CHSATRNK_trnK_27_	---AAGCTGTGTGCAAT---GAAA---AATGCAAGCACGGTTT--G	<u>55</u>

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CHMPXX_trnK_28_	----AAGCCGTATGCAGT----AAAA---ATTGCAAGTACGGTTT--G	56
CHNTXX_atpF_29_	----GAGCCAAATGAATC----GAAA---GATTCATGTTTGGTTC--G	57
CHPSATPC_atpF_30_	----GAGCCAAATGAATT----GAAA---GATTCATGTTTGGTTC--G	58
SOL400848_atpF_31_	----GAGCCAAATGAATT----GAAA---AATTCACGTTTGGTTC--G	59
CHTAATP1_atpF_32_	----GAGCCAAATGAATC----GAAA---GATTCATGTTTGGTTC--G	60
CHMPXX_atpF_33_	----AAGCCGAATGAATT----GAAA---AGTTCATGTTTCGGTTT--G	61
HVU010573_atp9_	----GAGCCAAATGAATC----GAAA---GATTCATGTTTGGTTC--G	62
CHNTXX_rpl2_34_	----AAGAAGTATGCTTT----GGAA---GAAGCTTGACAGTTT--G	63
CHMPXX_Cp_rpl2_	----AAGCTGTATGCTT----GAAA---AAAGCTTGACAGTTT--G	64
MIATGENA_rpl2_1_	----GAGCCGTACGAG-----GCAG-----CTCACGTACGGTTC--G	65
SCE011856_cytB_37_	----GAGCTGTATACTAT----GAAA---GTAGTACGTACAGTTC--T	66
CHNTXX_rps16_38_	----GAGCCGTACGAGGA----GAAA---GCTTCCTATACGTTTC--T	67
CHNTXX_rpoC1_39_	----GAGCCGGATGAAAG----GAAA---CTTTCACGTCCGATTT--T	68
SOL400848_rpoC1_40_	----GAGCCGGGCGAGGG----GAAA---CTTTCACGTCCGGCTT--T	69
CHMPXX_rpoC1_41_	----GAGCCGGATGACGG----AAAA---CTTTCATGTCCGATTC--T	70
CHMPXX_orf135_42_	----AAGCCATACAGAGTT----GAAA---ATATCATATATGGTTT--T	71
CHNTXX_petB_43_	----GAGCTGTACGAGAT----GAAA---GTCTCATATACGGTTC--T	72
SOL400848_petB_44_	----GAGCTGTACGAGAT----GAAA---GTCTCATATACAGTTC--T	73
CHZMXX_petB_45_	----GAGCCGTACGAGAT----GAAA---TTTTCATATACGGTTC--	74
CHMPXX_petB_46_	----AAGCTGTAAGATTA----TAAA---TAATCATTTACGGTTT--T	75
CHNTXX_petD_47_	----GAGCTGGATGATTA----AAAA---TTATCATGTCCAGTTC--C	76
SOL400848_petD_48_	----GAGCCGGATGATGA----AAAA---TTATCATGTCCGGTTC--T	77
CHZMXX_petD_49_	----GAGCCGGATGATGAA----AAA---TTCTCATGTCCGGTTC--C	78
CHMPXX_petD_50_	----GAGCCGGATGATAT----TAAA---TTATCATGTCCGATTC--T	79
CHNTXX_clpP_1_51_	----GAACCGTATGCATC----AAAA---GGCGCATGTACGGTTC--C	80
CHMPXX_clpP_1_52_	----AAGCTGTATGCGCTT----AAAA---AGTGCTTGACAGTTT--T	81
CHNTXX_ycf3_2_53_	----GAGCCGTATGAGGT----AAGAAA---TTCTCAAGTACGGTTC--T	82
CHNTXX_rpl16_54_	----GAGCTGGATGAGAA----GAAA---CTCTCACGTCCGGTTC--T	83
CHZMXX_rpl16_55_	----GAGCTGGATGAGAA----GAAA---CTCTCATGTCCAGTTT--T	84
CHSOL16_rpl16_56_	----GAGCCGGATGAGAA----GAAA---CTCTCATGTCCGGTTC--T	85
CHMPXX_rpl16_57_	----GAGCCGGATGAAT----CAAAA---TTTCATGTCCGGTTT--T	86
CHNTXX_ndh1_58_	----GAGCCGTATGAGAT----GAAA---ATCTCACGTACGGTTC--T	87
CHMPXX_ndh1_59_	----GAGCCGTATGAAAT----GAAA---ATTTTCATGTACGGTTT--T	88
CHNTXX_ndh2_60_	----GAGCCGTGTGAGAT----GAAA---GTCTCATGCACGGTTT--T	89
CHMPXX_ndh2_61_	----GAGCCGTGTGAATT----GAAA---ATCTCATGCACGGTTT--T	90
OBENAD202_nad2_4_	----GAGCCGTATGATGG----GCAA---CTATCTCCTGCGGTTC--G	91
CHNTXX_ycf3_1_62_	----GAGCCGTATGAGGT----GAAA---ATCTCACGTACGGTTC--T	92
CHMPXX_ycf3_1_63_	----GAGCCGTATGAAGT----TTAA---ACTTCATGTACGGTTT--T	93
CHNTXX_trnG_64_	----GAGCCGAATGAAAC----CAAA---GTTTCATGTTTCGGTTT--T	94
CHTATRN1_trnG_65_	----GAGCCGAATGAAAT----CAAA---ATTTTCATGTTTCGGTTT--T	95
CHMPXX_trnG_66_	----GAGCCGAATGAAAG----AAAA---CTTTCACGTTCGGTTT--T	96
MPOMTCG_trnG_	----GAGCCGGATGAGGGA----GAAA---TTTCTCACGTCCGGATC--T	97
CHNTXX_rps12_1_67_	----GAGCCGTATGAGGT----GAAA---ATCTCATGTACGGTTC--T	98
CHMPXX_rps12_1_68_	----AAGCCGTATGAAAT----GAAA---ATATCAAGTACGGTTT--T	99
CHZMXX_rps12_1_69_	----GAGCCGTATGAGGT----GAAA---ATCTCATGTACGGTTC--T	100
AMU41288_Am_rnl_	----GAGCCGTATGCGAT----GAAA---GTTGCACGTACGGTTC--T	101
AF029891_Cp_srRNA1	----GAGCCGTATGCGAT----GAAA---GTCGCACGTACGGTTC--T	102
TPSSRA_ssRNA	----GAGCCGTATGCGAT----GAAA---GTTGCACGTACGGTTC--T	103
AF087656_Aa_srRNA	----GAGCTGTATGCGAT----GAAA---GTCGCACGTACAGTTC--T	104

AF029891Cp_srRNA2	----GAGCCGTATGCCAT-----GAAA----GTGGCACGTACGGTTC--T	<u>105</u>
PLRRNA23_lrn_1	----CAGCCGTGTGCGGT-----GAAA----GTCGCACGCACGGTTG--T	<u>106</u>
PLRRNA23_lrn_2	----GAGCCGTGTGCGAT-----GAAA----GTCGCAAGCACGGTTC--T	<u>107</u>
PLRRNA23_lrn_3	----GAGCCGTGTGCGTT-----GAAA----GATGCATGCACGGTTC--T	<u>108</u>
PLRRNA23_lrn_4	----GAGCCGTATGAATG-----GAGA----CATTCACGTACGGTTT--T	<u>109</u>
MISOLSUR_rns2	----GAGCCGTGTGCGGT-----GAAA----GTCGCATGCACGGTTC--T	<u>110</u>
MPOMTCG_trnS	----GAGCCGTATGCGG-----GAAAA--CTCGCACGTACGGTTC--T	<u>111</u>
Azotobacter_Av_groEL	----GAGCCGTATGCGGG-----GAAA----CTCGCACGTACGGTTC--T	<u>112</u>
AF065404_Ba_pX01	----GAGCCGTATGTGCT-----GAAA----GGTACAAGTACGGTTC--	<u>113</u>
AB011549_Ec_IntE	----GAGCCGTATGCCGG-----GAAA----CTGGCACGTACGGTTC--T	<u>114</u>
PSY18999_Pp_Int5041C	----GAGCCGGATGAGGG-----GCCA--CTCTCATGTCCGGTTC--T	<u>115</u>
ECHREP_Ec_IntB	----GAGCGGTATGAGCC-----GAGA--GGTTCACGTACCGTTC--T	<u>116</u>
RMREVTM_Rm_Int1	----GAGCGGTGTGAATC-----GAGA--GGTTCACGCACCGTTC--T	<u>117</u>
ASU13767_An_hlyA	----GAGCCGTGTGCAGC-----GAAA--GTTGCACGCACGGATC--T	<u>118</u>
p	----GAGCCGTATGAGGT-----GAAA--GTCTCAAGTACGGTTT--T	<u>119</u>
LLU50902_Ll_ltrB	----GAGCCGTATACTCC-----GAGA--GGGGTACGTACGGTTC--C	<u>120</u>
PAU77945_Pa_Xin6	----CCGCCGTGTACG-----GAAC--CGTACGCACGGTGG--T	<u>121</u>
CDIIORF_Cd_orf14	----ACGCCGTGTGAGGG-----GAAA--CTCTCATGCACGGTGT--G	<u>122</u>
AB022308_Bm_TnpR	----ACGCCGTATGCTG-----GAAA--CTCGCCTGTACGGTGT--G	<u>123</u>
MTPLCOX1_cox1_1	----AAGCCGTATGAGGG-----GAAA--CTTTCACGTACGGTTT--G	<u>124</u>
MTPLCOX1_cox1_2	----GAGCCGTATGATGG-----GAAA--CTATCACGTACGGTTC--T	<u>125</u>
MTPLCOX1_cox1_3	----GAGCCCGGTGCGGT-----GAAA--GTCGCACGCCGGGTTC--G	<u>126</u>
SFU97489_Sf_IntA	----GAGCCGGATGCGCT-----GAAA--GGTGCACGTCCGGTTC--G	<u>127</u>

Please replace Table X at page 70 with the following table:

TABLE X
Corrected Sequence Information

Reference:

Sequence ID Number 1:

AI5gamma ----GAGCCGTATGCGAT-----GAAA----GTCGCACGTACGGTTC--T

Sequence ID Number [[43]] 44:

Before:

_ZPU16993_cox2 -----GAGCTTTTTCGCGG----GAAA----CTTGCAAGTCAAGTTT--G

After:

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_ZPU16993_cox2 ----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTCAAGTTT--G

Sequence ID Number [[52]] 53:

Before:

_BVSCOXIII1_cox2_1 -----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTACAGTTT--G

After:

_BVSCOXIII1_cox2_1 ----GAGCTTTTTGCGGG-----GAAA-----CTTGCAAGTACAGTTT--G